

## SEQUENCE LISTING

5 &lt;110&gt; Lunden, Anne

Andersson, Leif

Marklund, Stefan

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&lt;120&gt; Mutations in the FMO3 gene

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&lt;130&gt; Ref

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&lt;160&gt; 20

25 &lt;170&gt; PatentIn version 3.1

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35 &lt;213&gt; Artificial Sequence

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 Ala Ser Ile Tyr Arg Ser Val Phe Thr Asn Ser Ser Lys Glu Met Thr  
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15 tgt ttt cca gac ttt cca ttt cct gat gat ttt cct aac ttt atg cac 97  
 Cys Phe Pro Asp Phe Pro Phe Pro Asp Asp Phe Pro Asn Phe Met His  
 20 25 30

20 aac agc aag ctc cag gaa tat att act atg ttt gcc aaa gaa aag 142  
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&lt;213&gt; Bos taurus

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&lt;221&gt; exon

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 1 5 10 15

50 ctg ttt atc act cga ttt gaa aca ttc ctc aag aac acc tta ccg aca 97  
 Leu Phe Ile Thr Arg Phe Glu Thr Phe Leu Lys Asn Thr Leu Pro Thr  
 20 25 30

55 gtc att tct aac tgg tgg tac atg aag caa atg aac gcc aga ttc aag 145  
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			35				40					45						
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	Tyr	Ser	Tyr	Ala	Tyr	Pro	Phe	Leu	Asp	Asp	Ser	Ile	Ile	Lys	Ser	Arg		
35		50				55					60							
	gac	aat	gag	gtc	acc	tta	ttt	aaa	ggc	ata	ttc	cca	cct	cca	ctg	gaa	241	
	Asp	Asn	Glu	Val	Thr	Leu	Phe	Lys	Gly	Ile	Phe	Pro	Pro	Pro	Leu	Glu		
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	Lys	Pro	Thr	Leu	Ala	Val	Ile	Gly	Leu	Val	Gln	Ser	Leu	Gly	Ala	Ala		
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Phe Gly Lys Ser Asp Thr Ile Gln Thr Asp Tyr Val Val Tyr Met Asp
10   1           5           10           15

gag ctt gcc tcc ttc att ggg gca aag ccc aac atc cca tgg ctg ttt      97
Glu Leu Ala Ser Phe Ile Gly Ala Lys Pro Asn Ile Pro Trp Leu Phe
           20           25           30

15   ctc aca gat cca aag ttg gca ttg gag gtc tac ttt ggc cct tgc acc      145
Leu Thr Asp Pro Lys Leu Ala Leu Glu Val Tyr Phe Gly Pro Cys Thr
           35           40           45

20   cca tac cag ttt agg ctg gtg ggc cca gga aag tgg cca gga gcc aga      193
Pro Tyr Gln Phe Arg Leu Val Gly Pro Gly Lys Trp Pro Gly Ala Arg
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aac gcc atc      202
25 Asn Ala Ile
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&lt;212&gt; DNA

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&lt;220&gt;

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&lt;222&gt; (1) .. (714)

45 &lt;223&gt;

&lt;220&gt;

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&lt;221&gt; Intron

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    agctatgagc taaattcagc cattcaacaa atagttatca aggatatact tcgcacctga    180
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5   cccagaaaga ttaaatttca gaggagcttg ggaacacacg gatgtggact tctattttct    300
    agctcataca tcctctaaaa tgtaaggatg ccttccaata ggtggctcta ataaatgact    360
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    caacaaaagg atcgatgttg atttgcgtgg ataaaaagggt gtgaggcatt ttccctgttc    660
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    atc agt ggc ctg gcc tcc atc aga aac tgc cta gaa gag gga ctg gaa    98
    Ile Ser Gly Leu Ala Ser Ile Arg Asn Cys Leu Glu Glu Gly Leu Glu
    60      15          20          25
    ccc acc tgc ttt gag aag ggt gaa gac att ggg ggc ctg tgg aaa ttc    146

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	Ser	Asn	Trp	Trp	Tyr	Met	Lys	Gln	Met	Asn	Ala	Arg	Phe	Lys	His	Glu	
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15	agt tat gcc tac ccc ttc ctt gat gac tcc atc att aag agc aga gac	1058
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25	cca acc ttg gct gtg atc ggc ctt gtc cag tcc ctt gga gct gcc atc	1154
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Glu Gly Arg Ala Ser Ile Tyr Arg Ser Val Phe Thr Asn Ser Ser Lys  
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Thr Glu Lys Asp Gly Lys Lys Glu Ser Ala Val Phe Asp Ala Val Met  
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12/13

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